

CD105PCT ST25 (2).txt
SEQUENCE LISTING

<110> CropDesign N.V.

<120> Seedy1 sequence for making plants having changed growth characteristics

<130> CD-105-PCT

<150> US 60/528,113
<151> 2003-12-09

<150> EP 03104280.7
<151> 2003-11-19

<160> 18

<170> PatentIn version 3.3

<210> 1
<211> 1428
<212> DNA
<213> Nicotiana tabacum

<220>
<221> misc_feature
<223> seedy1 coding sequence (CDS0689)

<400> 1
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gcagcatttg ataatggaga ttctgaagat ttgtcttcgc tgaaacgttc ttggtctcct 120
ctgaaacccc tttcgggttag gccatcagat tcctttgaat ctgatttgtc aagtaaggaa 180
aatcaaactc ctttatttga gaattcatct gttaatctct catctccgtt acccataaag 240
ccacttaacc ctaatggggc tctggaaaat tcaagactca agccgaacaa gccaattcc 300
aaacagagtc ttgatgagat ggcggctaga aagagcggaa agggaaatga tttccgtgat 360
gagaagaaaa tagacgagga aattgaagaa attcagatgg agattagtag gttgagttca 420
agattagagg ctttgagaat tgaaaaggct gagaaaactg ttgctaagac tgttgaaaag 480
cgaggaaggg ttgtggcagc aaagtttatg gagccaaaac aaagtgttat taagattgaa 540
gagcgtatat caatgagtgc aagaacaaag gtggagcaga gaaggggtct tagtttagga 600
ccatctgaga tttttactgg aacgcggcgg cgagggttga gtatggggcc atcagatatt 660
ctagcagggg caacaaaggc acggcaattg ggaaagcaag agatgattat tactcctatt 720
cagccaatac aaaacaggcg aaagtcgtgt ttttggaagc ttcaagagat tgaagaagag 780
ggaaaaagtt caagccttag tcctaaatca agaaaaactg ctgcaagaac aatgggttaca 840
acaaggcagg cagttactac aattgcatca aagaagaatt tgaaaaaaga tgatgggactt 900
ttgagttcag ttcagccaaa gaagttgttt aaagatctcg aaaagtctgc tgctgctaata 960
aagaagcccc agaggccggg gagggttgtg gctagtaggt ataatacagag tacaattcag 1020

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tcatacagtag tgagaaagag gtctttacct gaaaatgata aggatgagag taagagaaat 1080
gataagaaac ggtcgttatc tgtagggaaa acgcgtgtgt ctcaaactga gagcaagaat 1140
ttgggtactg aaagtaggggt gaaaaagaga tgggaaattc ctagtgagat tgtagtcat 1200
ggaaacacag agagtggagaa atctccacta agcattattg tgaagcctga tttgcttccg 1260
cgaattagga ttgctcgggtg tgtgaatgag actcttaggg attctggacc tgctaaaaga 1320
atgatagagt tgataggcaa gaaatcgttt ttcagtagtg atgaagataa ggagccacct 1380
gtctgtcaag ttttaagttt tgcagaggaa gatgctgaag aggaataa 1428

```

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<210> 2
<211> 475
<212> PRT
<213> Nicotiana tabacum

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<220>
<221> MISC_FEATURE
<223> seedy1 protein (CDS0689)

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<400> 2

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Met Ser Val Leu Gln Tyr Pro Glu Gly Ile Asp Pro Ala Asp Val Gln
1          5          10          15

```

```

Ile Trp Asn Asn Ala Ala Phe Asp Asn Gly Asp Ser Glu Asp Leu Ser
          20          25          30

```

```

Ser Leu Lys Arg Ser Trp Ser Pro Leu Lys Pro Leu Ser Val Arg Pro
          35          40          45

```

```

Ser Asp Ser Phe Glu Ser Asp Leu Ser Ser Lys Glu Asn Gln Thr Pro
          50          55          60

```

```

Leu Phe Glu Asn Ser Ser Val Asn Leu Ser Ser Pro Leu Pro Ile Lys
          65          70          75          80

```

```

Pro Leu Asn Pro Asn Gly Ala Leu Glu Asn Ser Arg Leu Lys Pro Asn
          85          90          95

```

```

Lys Pro Asn Ser Lys Gln Ser Leu Asp Glu Met Ala Ala Arg Lys Ser
          100          105          110

```

```

Gly Lys Gly Asn Asp Phe Arg Asp Glu Lys Lys Ile Asp Glu Glu Ile
          115          120          125

```

```

Glu Glu Ile Gln Met Glu Ile Ser Arg Leu Ser Ser Arg Leu Glu Ala
          130          135          140

```

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Leu Arg Ile Glu Lys Ala Glu Lys Thr Val Ala Lys Thr Val Glu Lys
 145 150 155 160
 Arg Gly Arg Val Val Ala Ala Lys Phe Met Glu Pro Lys Gln Ser Val
 165 170 175
 Ile Lys Ile Glu Glu Arg Ile Ser Met Ser Ala Arg Thr Lys Val Glu
 180 185 190
 Gln Arg Arg Gly Leu Ser Leu Gly Pro Ser Glu Ile Phe Thr Gly Thr
 195 200 205
 Arg Arg Arg Gly Leu Ser Met Gly Pro Ser Asp Ile Leu Ala Gly Thr
 210 215 220
 Thr Lys Ala Arg Gln Leu Gly Lys Gln Glu Met Ile Ile Thr Pro Ile
 225 230 235 240
 Gln Pro Ile Gln Asn Arg Arg Lys Ser Cys Phe Trp Lys Leu Gln Glu
 245 250 255
 Ile Glu Glu Glu Gly Lys Ser Ser Ser Leu Ser Pro Lys Ser Arg Lys
 260 265 270
 Thr Ala Ala Arg Thr Met Val Thr Thr Arg Gln Ala Val Thr Thr Ile
 275 280 285
 Ala Ser Lys Lys Asn Leu Lys Lys Asp Asp Gly Leu Leu Ser Ser Val
 290 295 300
 Gln Pro Lys Lys Leu Phe Lys Asp Leu Glu Lys Ser Ala Ala Ala Asn
 305 310 315 320
 Lys Lys Pro Gln Arg Pro Gly Arg Val Val Ala Ser Arg Tyr Asn Gln
 325 330 335
 Ser Thr Ile Gln Ser Ser Val Val Arg Lys Arg Ser Leu Pro Glu Asn
 340 345 350
 Asp Lys Asp Glu Ser Lys Arg Asn Asp Lys Lys Arg Ser Leu Ser Val
 355 360 365
 Gly Lys Thr Arg Val Ser Gln Thr Glu Ser Lys Asn Leu Gly Thr Glu
 370 375 380
 Ser Arg Val Lys Lys Arg Trp Glu Ile Pro Ser Glu Ile Val Val His
 385 390 395 400

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Gly Asn Thr Glu Ser Glu Lys Ser Pro Leu Ser Ile Ile Val Lys Pro
405 410 415

Asp Leu Leu Pro Arg Ile Arg Ile Ala Arg Cys Val Asn Glu Thr Leu
420 425 430

Arg Asp Ser Gly Pro Ala Lys Arg Met Ile Glu Leu Ile Gly Lys Lys
435 440 445

Ser Phe Phe Ser Ser Asp Glu Asp Lys Glu Pro Pro Val Cys Gln Val
450 455 460

Leu Ser Phe Ala Glu Glu Asp Ala Glu Glu Glu
465 470 475

<210> 3
<211> 1336
<212> DNA
<213> Oryza sativa

<220>
<221> misc_feature
<223> seedy1 coding sequence

<400> 3
atggaggagg acccgctcat cccgctggtc cacgtctgga acaacgccgc cttcgacgac 60
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ggcgacaagg agaatcaccg ccccgagggt gttgatgtcg ccgccggcta cgacgtcgag 180
gccgagatcg gccacatcga ggcggagatc ctgcgcctct cgtcccggct ccaccatctc 240
cgcgtctcca agcagccgga gccaaccgc gacgacgctc cgatggggga gatggtcgcg 300
aaggtgaggc cccggccgag gggcctcagc ctcgggcccc tggatgtgat ctccatcgtc 360
aatcgtgaga agcatccgct gcgcaccaag cagcctccgg cgacgcgggg cagggggctc 420
agcctcgggc ccatggagat cgccgcggcg aaccctaggg tgcccgcggc ggcgagcat 480
cagcaacagc aacgcgctgg cagggcgcgg atcctgaagc caatcaagga gcctccggtg 540
cagcgtcgca ggggcgtcag cctcgggccg ttggagatcc accacggcgt cggcagcaag 600
gcaccagcgg cggcgcgagc caagccgttc accaccaagc tcaacgccat tcgagaagaa 660
acccgaccct ccaagcaatt cgccgtcccc gccaaagccat ggccgtcgag caatacaagg 720
cagacactgg actcgaggca aggaacagca gcaagtcgag cgaaggcgag gagcccgagc 780
cccaggccca ggaggcaatc caatggcaag gctactgaca caaggggagg caacaagggtg 840
gtggatgagc tcaagcccaa aggtgcgtcg tcaagtcaga gcggcagcgc cgccgccgcc 900

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gccactgccca agaggatggc ggggagctcc aagatgaggg tcatcccgag ccgctacagc 960
ctcactcctg gcgcttcctt tggaagcagt ggagcacagg agaggcgacg caagcagtct 1020
ctcccaggat catcagggga tgcgaaccag aatgaggaaa tcagagcgaa ggtcatcgag 1080
ccttccaatg atccactctc tcctcaaacg atctccaagg ttgctgaaat gctcccaaag 1140
atcaggacca tgccgcctcc tgacgagagc cctcgcgatt ccggatgcgc caagcggggtt 1200
gccgaattgg tcgggaagcg ctcgttcttc acggctgcag ccgaggacgg gcgggcgctc 1260
gacgtcgaag cacccgaggc ggtcgcagaa gcttgagatg aaccaccatg gtttgatccg 1320
ttccttccat cagctc 1336

<210> 4
<211> 431
<212> PRT
<213> Oryza sativa

<220>
<221> MISC_FEATURE
<223> seedy1 protein

<400> 4

Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
1 5 10 15

Ala Phe Asp Asp Ser Ser Cys Ser Arg Ser Ala Trp Leu Pro Gln Ser
20 25 30

Pro Ala Val Ala Ala Val Arg Lys Gly Asp Lys Glu Asn His Arg Pro
35 40 45

Glu Val Val Asp Val Ala Ala Gly Tyr Asp Val Glu Ala Glu Ile Gly
50 55 60

His Ile Glu Ala Glu Ile Leu Arg Leu Ser Ser Arg Leu His His Leu
65 70 75 80

Arg Val Ser Lys Gln Pro Glu Pro Asn Arg Asp Asp Ala Pro Met Gly
85 90 95

Glu Met Val Ala Lys Val Arg Pro Arg Pro Arg Gly Leu Ser Leu Gly
100 105 110

Pro Leu Asp Val Ile Ser Ile Val Asn Arg Glu Lys His Pro Leu Arg
115 120 125

Thr Lys Gln Pro Pro Ala Thr Arg Gly Arg Gly Leu Ser Leu Gly Pro
130 135 140

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Met Glu Ile Ala Ala Ala Asn Pro Arg Val Pro Ala Ala Ala Gln His
145 150 155 160

Gln Gln Gln Gln Arg Ala Gly Thr Ala Arg Ile Leu Lys Pro Ile Lys
165 170 175

Glu Pro Pro Val Gln Arg Arg Arg Gly Val Ser Leu Gly Pro Leu Glu
180 185 190

Ile His His Gly Val Gly Ser Lys Ala Pro Ala Ala Ala Arg Ala Lys
195 200 205

Pro Phe Thr Thr Lys Leu Asn Ala Ile Arg Glu Glu Thr Arg Pro Ser
210 215 220

Lys Gln Phe Ala Val Pro Ala Lys Pro Trp Pro Ser Ser Asn Thr Arg
225 230 235 240

Gln Thr Leu Asp Ser Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala
245 250 255

Arg Ser Pro Ser Pro Arg Pro Arg Arg Gln Ser Asn Gly Lys Ala Thr
260 265 270

Asp Thr Arg Gly Gly Asn Lys Val Val Asp Glu Leu Lys Pro Lys Gly
275 280 285

Ala Ser Ser Ser Gln Ser Gly Ser Ala Ala Ala Ala Ala Thr Ala Lys
290 295 300

Arg Met Ala Gly Ser Ser Lys Met Arg Val Ile Pro Ser Arg Tyr Ser
305 310 315 320

Leu Thr Pro Gly Ala Ser Leu Gly Ser Ser Gly Ala Gln Glu Arg Arg
325 330 335

Arg Lys Gln Ser Leu Pro Gly Ser Ser Gly Asp Ala Asn Gln Asn Glu
340 345 350

Glu Ile Arg Ala Lys Val Ile Glu Pro Ser Asn Asp Pro Leu Ser Pro
355 360 365

Gln Thr Ile Ser Lys Val Ala Glu Met Leu Pro Lys Ile Arg Thr Met
370 375 380

Pro Pro Pro Asp Glu Ser Pro Arg Asp Ser Gly Cys Ala Lys Arg Val

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395

385

390

400

Ala Glu Leu Val Gly Lys Arg Ser Phe Phe Thr Ala Ala Ala Glu Asp
405 410 415

Gly Arg Ala Leu Asp Val Glu Ala Pro Glu Ala Val Ala Glu Ala
420 425 430

```
<210> 5
<211> 1860
<212> DNA
<213> Medicago truncatula
```

```
<220>
<221> misc_feature
<223> seedy1 coding sequence
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<400>	5						
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aatcacatcg	gagcgtgtat	gagtagccgt	ttcacatcca	acggccagta	agagcgtaac		180
tttattttctt	ccctcttcaa	tctccaacgg	tcacataatc	tcttccaaat	acaaataatt		240
ccctcttttca	acctcactct	tcattttctt	aaccctaaacc	caaaaaacta	atcagattct		300
tcttaaatct	tgaaaccttt	ctcccaaaag	cacttaaata	aaaaagcact	taaccatgaa		360
taacacaaac	aacaacaaca	ttctttcttca	ttccacacag	gttcaagtgt	ggaacaacgc		420
agcattcgat	ggtgaagatt	tcgccatgaa	ttcatcttct	gattccatca	aagagaatct		480
aaacccatcc	gcattcaaca	ttgttccttc	ttcaaacaaa	agaactattg	atgatgaaat		540
tgcggaat	gaaagtga	ttaagcgatt	aacttcgaag	ctggaattgc	ttcgtgttga		600
aaaagctgaa	agaaaaatcg	cttctgaaaa	gcgtgttagt	ggaattggta	ctggaagaat		660
agtagcagcg	aagtttatgg	aaccgaagaa	aaacgttaca	ccgaaacgaa	acggtgtcgt		720
tttcaaggag	gagacaccga	aacgaaacgg	tgctgtttcg	gatacgccga	aatctagggt		780
taattggaga	agagggatga	gtttaggtcc	gatggagatt	gccgggaaag	tgatggcacc		840
gccggcgatg	acgattactc	cggcgacggt	gaatcggagg	aagtcttggt	tctggaaacc		900
gcaggaaagt	tgtgaagtaa	tgccgtcggg	gattactccg	gcgacggtga	ataggaggaa		960
atcttgtttt	ttgaaacctc	aagaaagttg	tgaagaaaat	cgaagaaaaa	cgatttgcaa		1020
accgaatttg	aatttgaatt	caaattcagt	taattctgcg	gttggatcga	ttaagcgtgt		1080
gaagaagaaa	gatgaagaaa	ttgctcaggt	tcaaccgaag	aagctgtttg	aaggtgaaaa		1140
atcagtgaag	aaatcgttga	aacaaggtag	aattgttgca	agccggtata	attccggtgg		1200
tggtggtggt	gatgagagga	aaagatcggt	ttcggagaat	aataaggggt	tagggagtga		1260

CD105PCT ST25 (2).txt

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aatcagggct aagaagagat gggagatacc aattgaagaa gtggatgtga gtggttttgt 1320
tatgtttaccg aagatttcga caatgagggt tgttgatgag agtcctagag attctggtgc 1380
tgttaaaaga gttgctgaat tgaatggaaa aagatcttac ttttgtgatg aagatgagga 1440
ggagagagtg atggtggagg aagaagggtg ttctgtttgt caggttttga attttgctga 1500
agatgatgat gatgatgatg attatggtga acaagggtaa ttgtggaaat tggaattgat 1560
ttgtttttgt ggggtttgtg ggaactggct atgttctgct tgattctttt gcattttggt 1620
gtgaaactaa agatgagggtg aaaagtttat gcttgttaaa ttggattggt ttatatgttt 1680
tgaaataata acaacaagca tgtgtcttgc ttaataattg tatattgttt tgtttgtttt 1740
ataatgatat ggatttaatt tgtatacaca atataatata gtatgcattg agagagtttt 1800
tcgttcagta ttcattctga ttttagtggt tatctcattc tagaagattg tattttgttg 1860

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<210> 6
 <211> 394
 <212> PRT
 <213> Medicago trunculata

<220>
 <221> MISC_FEATURE
 <223> seedy1 protein
 <400> 6

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Met Asn Asn Thr Asn Asn Asn Asn Ile Leu Leu His Ser Thr Gln Val
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Gln Val Trp Asn Asn Ala Ala Phe Asp Gly Glu Asp Phe Ala Met Asn
20      25      30

Ser Ser Ser Asp Ser Ile Lys Glu Asn Leu Asn Pro Ser Ala Phe Asn
35      40      45

Ile Val Pro Ser Ser Asn Lys Arg Thr Ile Asp Asp Glu Ile Ala Glu
50      55      60

Ile Glu Ser Glu Ile Lys Arg Leu Thr Ser Lys Leu Glu Leu Leu Arg
65      70      75      80

Val Glu Lys Ala Glu Arg Lys Ile Ala Ser Glu Lys Arg Val Ser Gly
85      90      95

Ile Gly Thr Gly Arg Ile Val Ala Ala Lys Phe Met Glu Pro Lys Lys
100     105     110

Asn Val Thr Pro Lys Arg Asn Gly Val Val Phe Lys Glu Glu Thr Pro

```


CD105PCT ST25 (2).txt

115

120

125

Lys Arg Asn Gly Val Val Ser Asp Thr Pro Lys Ser Arg Val Asn Trp
 130 135 140

Arg Arg Gly Met Ser Leu Gly Pro Met Glu Ile Ala Gly Lys Val Met
 145 150 155 160

Ala Pro Pro Ala Met Thr Ile Thr Pro Ala Thr Val Asn Arg Arg Lys
 165 170 175

Ser Cys Phe Trp Lys Pro Gln Glu Ser Cys Glu Val Met Pro Ser Gly
 180 185 190

Ile Thr Pro Ala Thr Val Asn Arg Arg Lys Ser Cys Phe Leu Lys Pro
 195 200 205

Gln Glu Ser Cys Glu Glu Asn Arg Arg Lys Thr Ile Cys Lys Pro Asn
 210 215 220

Leu Asn Leu Asn Ser Asn Ser Val Asn Ser Ala Val Gly Ser Ile Lys
 225 230 235 240

Arg Val Lys Lys Lys Asp Glu Glu Ile Ala Gln Val Gln Pro Lys Lys
 245 250 255

Leu Phe Glu Gly Glu Lys Ser Val Lys Lys Ser Leu Lys Gln Gly Arg
 260 265 270

Ile Val Ala Ser Arg Tyr Asn Ser Gly Gly Gly Gly Gly Asp Ala Arg
 275 280 285

Lys Arg Ser Phe Ser Glu Asn Asn Lys Gly Leu Gly Ser Glu Ile Arg
 290 295 300

Ala Lys Lys Arg Trp Glu Ile Pro Ile Glu Glu Val Asp Val Ser Gly
 305 310 315 320

Phe Val Met Leu Pro Lys Ile Ser Thr Met Arg Phe Val Asp Glu Ser
 325 330 335

Pro Arg Asp Ser Gly Ala Val Lys Arg Val Ala Glu Leu Asn Gly Lys
 340 345 350

Arg Ser Tyr Phe Cys Asp Glu Asp Glu Glu Glu Arg Val Met Val Glu
 355 360 365

CD105PCT ST25 (2).txt

Glu Glu Gly Gly Ser Val Cys Gln Val Leu Asn Phe Ala Glu Asp Asp
 370 375 380

Asp Asp Asp Asp Asp Tyr Gly Glu Gln Gly
 385 390

<210> 7
 <211> 674
 <212> DNA
 <213> Saccharum sp.

<220>
 <221> misc_feature
 <223> seedy1 coding sequence (partial 5' end)

<220>
 <221> misc_feature
 <222> (362)..(362)
 <223> n can be a, c, g or t

<220>
 <221> misc_feature
 <222> (372)..(372)
 <223> n can be a, c, g or t

<220>
 <221> misc_feature
 <222> (674)..(674)
 <223> n can be a, c, g or t

<400> 7
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 gaagcaggaa tccctccgct cccagccgcc tcctccgctc acccatcgat cgatcggtccg 120
 tccggtccag ggggctctcc ggcggcggtg gcgatggagg aggacccgct catcccgtg 180
 gtgcacgtct ggaacaacgc cgccttcgac cagcctcct cctccgcgtg gcacgcccac 240
 tcccctgtgc ccgcgagcgc acgtcgcgag gcggaggggg acaaggagaa ccaccgcccc 300
 gaccccgacc ccgacgtcga ggcggagatc ggccacatcg aggcgagat cctgcgctg 360
 tncctccgcc tncaccacct tcgcacctcc aagcagtcgg agccgtccaa gcgcggagag 420
 gtcgcgcccc cgcccgcggc gaaggcgaaa gcggcgggcg cggcgcggct gcggacgcgg 480
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 gacaaccagc agcagcagcc gcgtgccgcg caggggtctga agccgatcaa gcaggccacg 600
 gcggcgggcg gcaagggcgt aagacttggg ccccttcgac atggtcggcg cgaaccctag 660
 ggtccctccg ccn 674

<210> 8
 <211> 166
 <212> PRT
 <213> Saccharum sp.

CD105PCT ST25 (2).txt

<220>
<221> MISC_FEATURE
<223> seedy1 protein

<220>
<221> MISC_FEATURE
<223> seedy1 protein (partial N term)

<220>
<221> MISC_FEATURE
<222> (70)..(70)
<223> Xaa can be any amino acid

<400> 8

Met Glu Glu Asp Pro Leu Ile Pro Leu Val His Val Trp Asn Asn Ala
1 5 10 15

Ala Phe Asp His Ala Ser Ser Ser Ala Trp His Ala His Ser Pro Val
20 25 30

Pro Ala Ser Ala Arg Arg Glu Ala Glu Gly Asp Lys Glu Asn His Arg
35 40 45

Pro Asp Pro Asp Pro Asp Val Glu Ala Glu Ile Gly His Ile Glu Ala
50 55 60

Glu Ile Leu Arg Leu Xaa Ser Arg Leu His His Leu Arg Thr Ser Lys
65 70 75 80

Gln Ser Glu Pro Ser Lys Arg Gly Glu Val Ala Pro Ala Pro Ala Ala
85 90 95

Lys Ala Lys Ala Ala Ala Ala Arg Leu Arg Thr Arg Gly Leu Ser
100 105 110

Leu Gly Pro Leu Asp Val Ala Ala Ala Gly Asn Pro Asn Pro Leu Thr
115 120 125

Thr Asp Asn Gln Gln Gln Gln Pro Arg Ala Ala Gln Gly Leu Lys Pro
130 135 140

Ile Lys Gln Ala Thr Ala Ala Ala Gly Lys Gly Val Arg Leu Gly Pro
145 150 155 160

Leu Arg His Gly Arg Arg
165

<210> 9
<211> 876

CD105PCT ST25 (2).txt

<212> DNA
<213> Zea mays

<220>
<221> misc_feature
<223> seedy1 coding sequence (partial 3' end)

<220>
<221> misc_feature
<222> (869)..(869)
<223> n = a, c, g or t

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caagcagagc caaggcgagg agcgggagca taagccccag caggttcagg aggcagtcca      180
cttccaaggc tgccgagaca agagcgggaa atgccaagcc tacagaggcg acgaggggag      240
ggagcgaagc ggtcaatcac accagcaatg tagccacgac gaagaggccg gcggggagct      300
ccaagggtcag ggttgtcccc agccgtaca gcatcccacc tggctcctcc ctagcagctg      360
tgacacaagg caaccgatgc aagcagtctc tcccaggatc ggctactgag accagagtaa      420
atctcactga gccgccgaac gacgagttgt ctctgaaga acttgccaag gttgcagagc      480
tgctcccaag gattaggacc atgccgcctt ctgatgagag cccgcgtgac tcgggatgtg      540
ccaagcgtgt tgctgatttg gtcgggaagc gatccttctt cactgctgca ggggacgatg      600
gcaatctcgt tacgccctac caggcacggg tggttgaact tgaatcaccg gaggcagcag      660
cagaagaagc agaagcttga gaagtttgtc tttgatcaat tccgaagtgg cttgcatctg      720
ggcgtggcct ctttttgcag tgtgtgctac tacatagtct actgttacat tcatatcata      780
tcacatttcc ttttttttcc cccttgagac attgcttagt acttttgtgt tgccttgtga      840
aaagagagtg gaaggttcat ctgctgatnc cttggtt                                876

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<210> 10
<211> 224
<212> PRT
<213> Zea mays

<220>
<221> MISC_FEATURE
<223> seedy1 protein (partial C term)

<400> 10

Thr Arg Pro Ala Val Arg Glu Glu Glu Gly Gln Arg Ser Lys Glu His
1 5 10 15

Ala Val Pro Ala Arg Pro Trp Pro Ser Ser Asn Ala Arg His Pro Leu
20 25 30

CD105PCT ST25 (2).txt

Asp Ala Arg Gln Gly Thr Ala Ala Ser Arg Ala Lys Ala Arg Ser Gly
35 40 45

Ser Ile Ser Pro Ser Arg Phe Arg Arg Gln Ser Thr Ser Lys Ala Ala
50 55 60

Glu Thr Arg Ala Gly Asn Ala Lys Pro Thr Glu Ala Thr Arg Gly Gly
65 70 75 80

Ser Glu Ala Val Asn His Thr Ser Asn Val Ala Thr Thr Lys Arg Pro
85 90 95

Ala Gly Ser Ser Lys Val Arg Val Val Pro Ser Arg Tyr Ser Ile Pro
100 105 110

Pro Gly Ser Ser Leu Ala Ala Val Thr Gln Gly Asn Arg Cys Lys Gln
115 120 125

Ser Leu Pro Gly Ser Ala Thr Glu Thr Arg Val Asn Leu Thr Glu Pro
130 135 140

Pro Asn Asp Glu Leu Ser Pro Glu Glu Leu Ala Lys Val Ala Glu Leu
145 150 155 160

Leu Pro Arg Ile Arg Thr Met Pro Pro Ser Asp Glu Ser Pro Arg Asp
165 170 175

Ser Gly Cys Ala Lys Arg Val Ala Asp Leu Val Gly Lys Arg Ser Phe
180 185 190

Phe Thr Ala Ala Gly Asp Asp Gly Asn Leu Val Thr Pro Tyr Gln Ala
195 200 205

Arg Val Val Glu Leu Glu Ser Pro Glu Ala Ala Ala Glu Glu Ala Glu
210 215 220

<210> 11
<211> 1257
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> misc_feature
<223> seedy1 coding sequence

<400> 11
atgacatcaa ttgaggcaac agaaacgctt aacgctcctc caaagcttca gatctggaac 60

CD105PCT_ST25 (2).txt

```

aacgctgcct tcgacgatgg agattctcaa atcacttccg ccatcgaagc ttcttcttgg 120
tctcacctca acgaatcatt cgattccgat tgtagcaagg agaatcagtt tccgatttcg 180
gtttcctctt cgctccaatc ctcagtctcg atcaccgaag ctccgtcagc aaaatccaag 240
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gaagaagtag agaaggagat cggacgatta tcgacgaaat tggagtcgct ccgattagag 360
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 35 40 45

CD105PCT ST25 (2).txt

Ser Asp Cys Ser Lys Glu Asn Gln Phe Pro Ile Ser Val Ser Ser Ser
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Leu Gln Ser Ser Val Ser Ile Thr Glu Ala Pro Ser Ala Lys Ser Lys
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Thr Val Lys Thr Lys Ser Ala Ala Asp Arg Ser Lys Lys Arg Asp Ile
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Asp Ala Glu Ile Glu Glu Val Glu Lys Glu Ile Gly Arg Leu Ser Thr
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Lys Leu Glu Ser Leu Arg Leu Glu Lys Ala Glu Gln Thr Ala Arg Ser
115 120 125

Ile Ala Ile Arg Gly Arg Ile Val Pro Ala Lys Phe Met Glu Ser Ser
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Gln Lys Gln Val Lys Phe Asp Asp Ser Cys Phe Thr Gly Ser Lys Ser
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Arg Ala Thr Arg Arg Gly Val Ser Leu Gly Pro Ala Glu Ile Phe Asn
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Ser Ala Lys Lys Ser Glu Thr Val Thr Pro Leu Gln Ser Ala Gln Asn
180 185 190

Arg Arg Lys Ser Cys Phe Phe Lys Leu Pro Gly Ile Glu Glu Gly Gln
195 200 205

Val Thr Thr Arg Gly Lys Gly Arg Thr Ser Leu Ser Leu Ser Pro Arg
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Ser Arg Lys Ala Lys Met Thr Ala Ala Gln Lys Gln Ala Ala Thr Thr
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Val Gly Ser Lys Arg Ala Val Lys Lys Glu Glu Gly Val Leu Leu Thr
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Ile Gln Pro Lys Arg Leu Phe Lys Glu Asp Glu Lys Asn Val Ser Leu
260 265 270

Arg Lys Pro Leu Lys Pro Gly Arg Val Val Ala Ser Arg Tyr Ser Gln
275 280 285

Met Gly Lys Thr Gln Thr Gly Glu Lys Asp Val Arg Lys Arg Ser Leu
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295

Pro Glu Asp Glu Glu Lys Glu Asn His Lys Arg Ser Glu Lys Arg Arg
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Ala Ser Asp Glu Ser Asn Lys Ser Glu Gly Arg Val Lys Lys Arg Trp
325 330 335

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Glu Ser Pro Ile Val Lys Glu Leu Pro Lys Ile Arg Thr Leu Arg Arg
355 360 365

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CD105PCT ST25 (2).txt

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CD105PCT ST25 (2).txt

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CD105PCT ST25 (2).txt

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CD105PCT ST25 (2).txt

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